

Genome-wide identification and expression profiling of growth-regulating factor (GRF) and GRF-interacting factor (GIF) gene families in chickpea and pigeonpea

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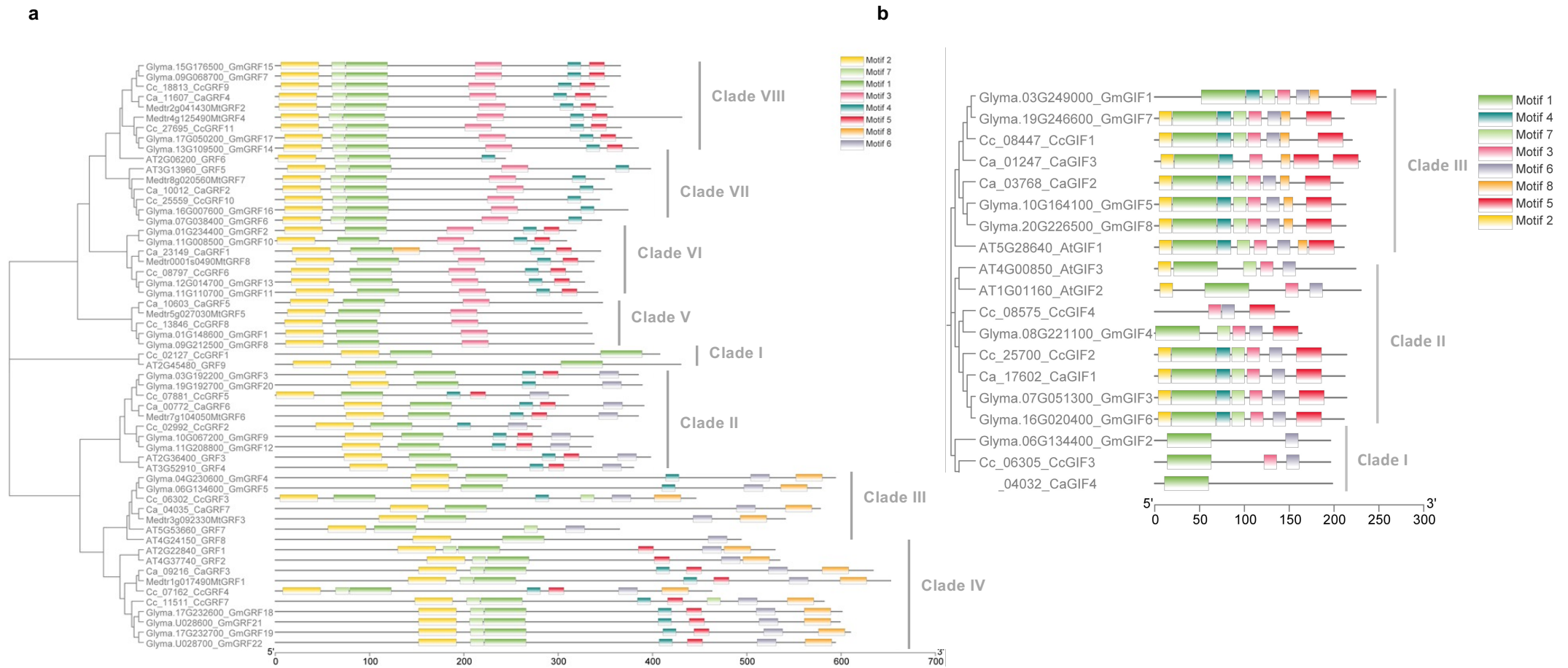


Fig. S2 Motif analysis of identified GRF and GIF proteins. (a) Motif analysis of 7 CaGRF, 11 CcGRF, 22 GmGRF, 8 MtGRF and 9 AtGRF proteins (b) Motif analysis of 4 CcGIF, 4 CaGIF, 8 GmGIF and 3 AtGIF proteins. Motif analysis was conducted using MEME online tool with maximum 8 motifs to be identified

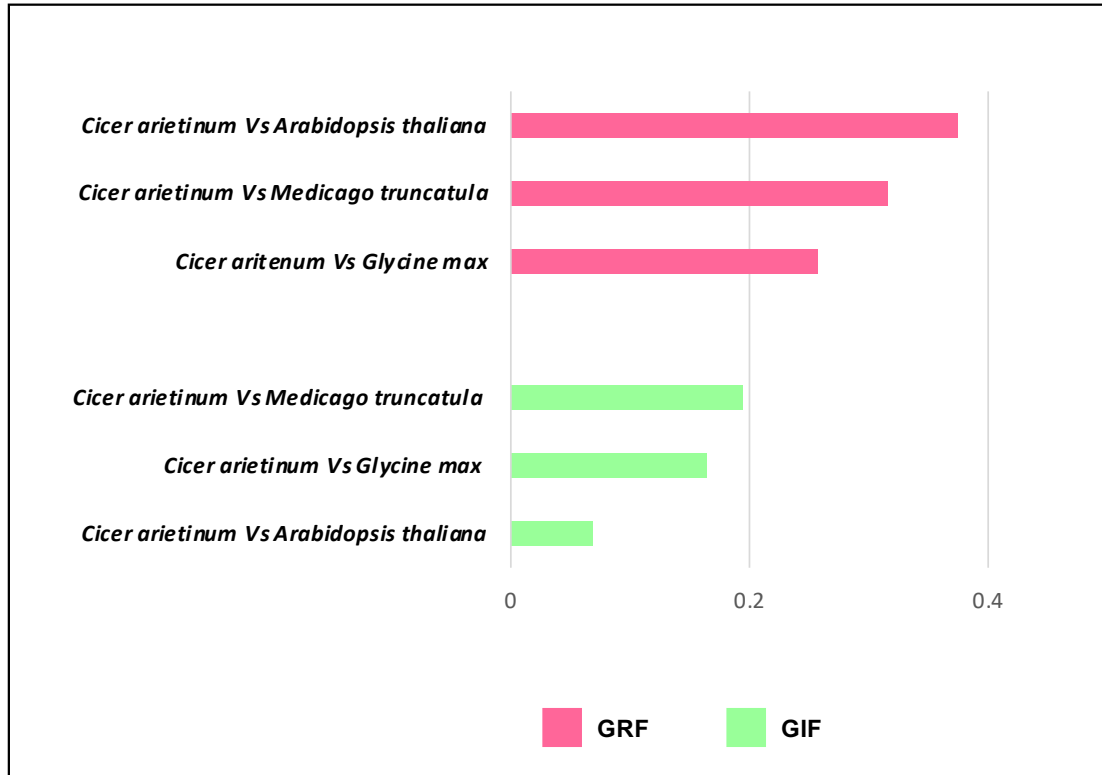
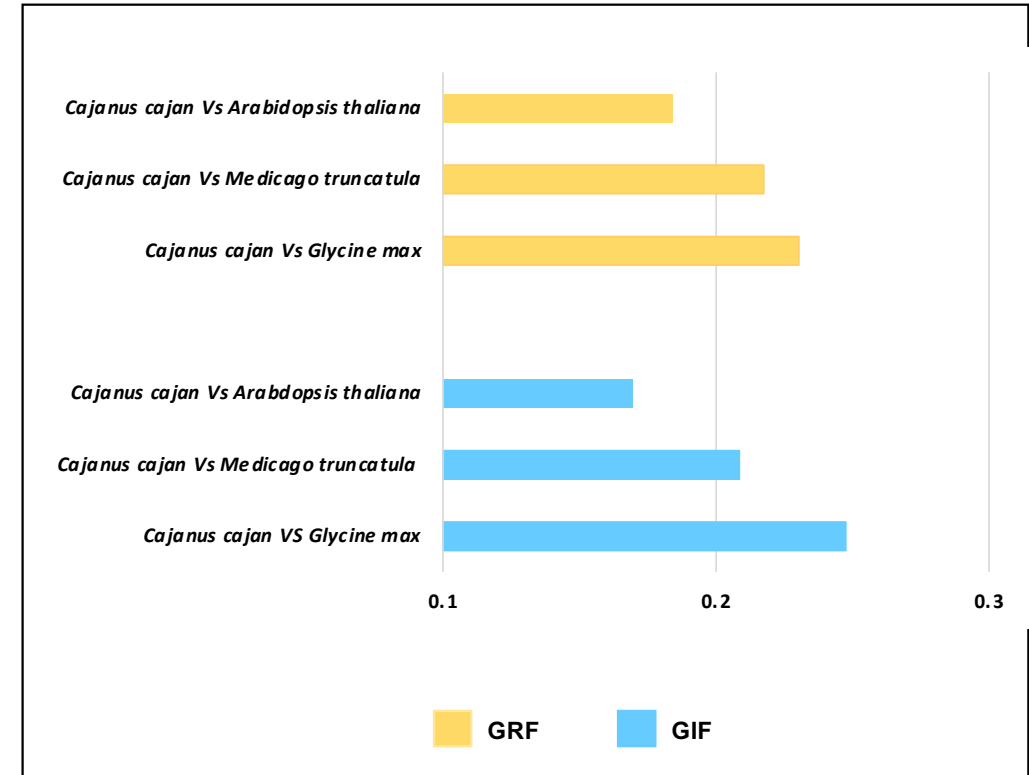
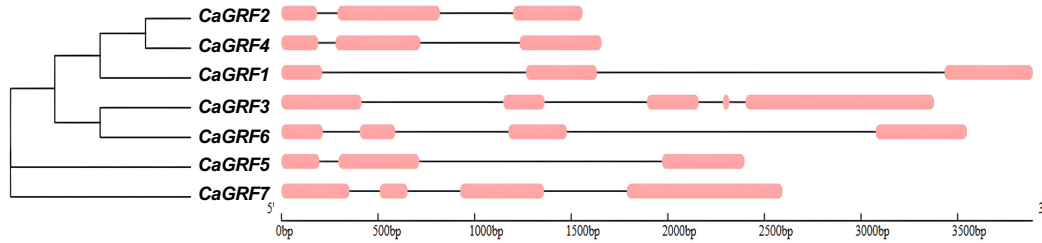
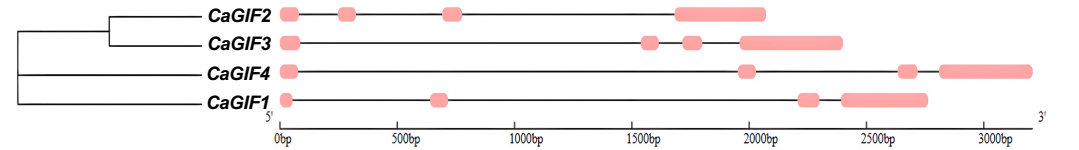
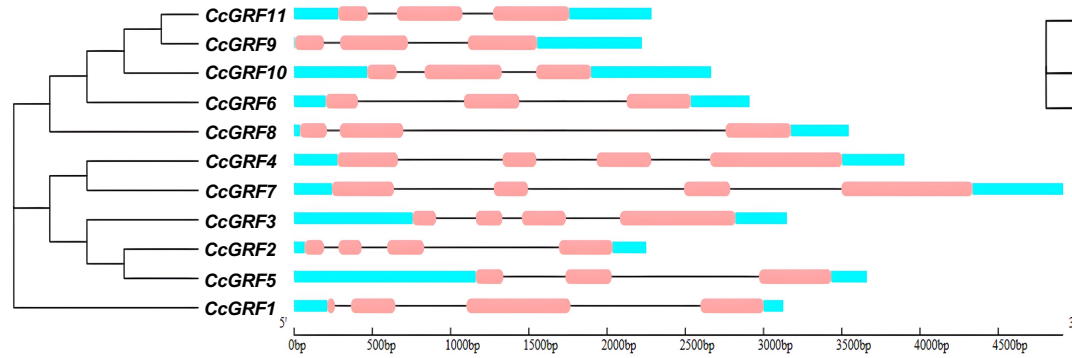
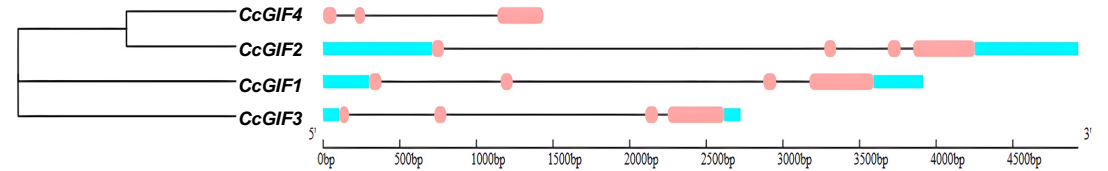
a**b**

Fig. S3 Ka/Ks ratios of GRF and GIF genes. **a**, Graph representing average Ka/Ks ratios of collinear gene pairs of GRF as well as GIF genes from *Cicer arietinum*, *Glycine max*, *Medicago truncatula* and *Arabidopsis thaliana*. **b**, Graph representing average Ka/Ks ratios of collinear gene pairs of GRF as well as GIF genes from *Cajanus cajan*, *Glycine max*, *Medicago truncatula* and *Arabidopsis thaliana*

a**b****c****d**

Exon Intron Upstream/ Downstream

Fig. S4 Gene structures of *GRF* and *GIF* genes. **a**, Gene structures of *CaGRF* genes. **b**, Gene structures of *CaGIF* genes. **c**, Gene structures of *CcGRF* genes. **d**, Gene structures of *CcGIF* genes. Exons are represented as pink boxes, and introns are represented as black lines while untranslated regions (UTRs) are represented as blue boxes

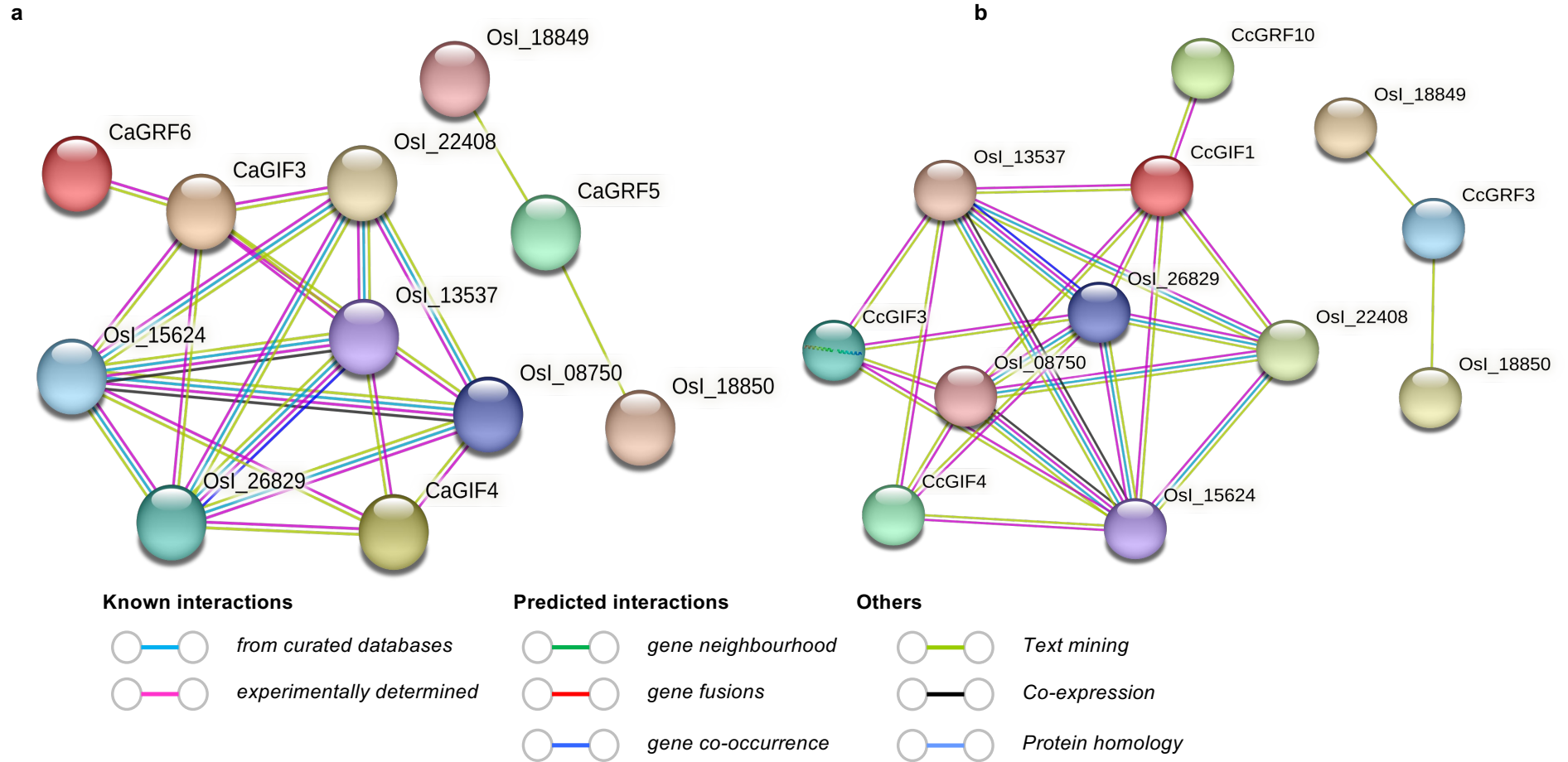


Fig. S6 Predicted protein interaction networks of **a**, CaGRF and GIF proteins, **b** CcGRF and GIF proteins based on their homology with *Oryza sativa* GRF-GIF proteins obtained from STRING database. The type of interactions between the proteins is represented by different coloured lines as described in the figure legend. Red line indicates the presence of fusion evidence; Green line is neighborhood evidence; Blue line is co-occurrence evidence; Purple line is experimental evidence; Yellow line—text mining evidence; Light blue line—database evidence; Black line—co-expression evidence